AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (Original) Purified or isolated nucleic acid of the SPG4 gene, characterized in that it comprises a sequence chosen from the group comprising:

a) the sequence SEQ ID No. 1, the sequence SEQ ID No. 2, the sequence SEQ ID No. 72, the sequence SEQ ID No. 106 or the sequence of at least 15 consecutive nucleotides of one of these sequences;

b) the nucleic acid sequences which are homologs or variants of the sequences SEQ ID No. 1, SEQ ID No. 2, SEQ ID No. 72 or SEQ ID No. 106; and

c) the complementary sequence or the RNA sequence corresponding to the sequences as defined in a) and b).

2. (Original) Purified or isolated nucleic acid according to claim 1, with the exception of the nucleic acid identified in the GenBank databank under the accession number AB029006.

3. (Previously Presented) Purified or isolated nucleic acid according to claim 1, characterized in that it comprises at least one sequence of at least 15 consecutive

nucleotides of the nt 714-809, ends inclusive, fragment of the sequence SEQ ID No. 2, of the sequence complementary thereto or of the sequence of the corresponding RNA thereof.

4. (Previously Presented) Purified or isolated nucleic acid according to claim 1, characterized in that it comprises a mutation corresponding to a natural polymorphism in humans.

5. (Previously Presented) Probe or primer, characterized in that it comprises a sequence of a nucleic acid according to claim 1.

6. (Original) Probe or primer according to claim 5, characterized in that its sequence is chosen from the sequences SEQ ID No. 4 to SEQ ID No. 71.

7. (Original) Splice acceptor or donor site, characterized in that it comprises a sequence of a nucleic acid according to claim 1 chosen from the sequences SEQ ID No. 74 to SEQ ID No. 105.

8. (Previously Presented) Method for screening cDNA or genomic DNA libraries, or for cloning isolated genomic or cDNA encoding spastin, characterized in that it uses a nucleic acid sequence according to claim 1.

9. (Previously Presented) Method according to claim 8, for identifying the genomic or cDNA sequence of the SPG4 gene of mammals.

10. (Currently Amended) ~~Method~~ A method for identifying a mutation carried by the human SPG4 gene, characterized in that it uses a nucleic acid sequence according to claim 1.

11. (Currently Amended) ~~Method~~ A method according to claim 10, for identifying a mutation responsible for autosomal dominant hereditary spastic paraplegia.

12. (Previously Presented) Method for identifying the nucleic acid sequences which promote and/or regulate the expression of the SPG4 gene, characterized in that it uses a nucleic acid sequence according to claim 1.

13. (Previously Presented) Nucleic acid identified using a method according to claim 9.

14. (Previously Presented) Polypeptide encoded by a nucleic acid according to claim 1.

15. (Previously Presented) Polypeptide according to claim 14, with the exception of the 584 amino acid peptide, the sequence of which is identified in the GenBank databank under the accession number AB029006.

16. (Previously Presented) Polypeptide according to claim 14, characterized in that it comprises an amino acid sequence chosen from the group comprising:

a) the sequence SEQ ID No. 3, the sequence SEQ ID No. 73, the sequence SEQ ID No. 107 or the sequence of at least 10 consecutive amino acids of one of these sequences; and

b) the sequences which are homologs or variants of the sequences SEQ ID No. 3, SEQ ID No. 73 or SEQ ID No. 107.

17. (Previously Presented) Polypeptide according to claim 14, characterized in that it comprises the sequence of at least 8 consecutive amino acids of the sequence of the aa 197-228, ends inclusive, fragment of the sequence SEQ ID No. 3.

18. (Previously Presented) Polypeptide according to claim 14, characterized in that it comprises an amino acid sequence chosen from the group comprising the sequence

SEQ ID No. 3, the sequence SEQ ID No. 73, the sequence SEQ ID No. 107, which sequences carrying at least one of the mutations corresponding to a natural polymorphism in humans, and the sequences of the fragments thereof of at least 10 consecutive amino acids.

19. (Previously Presented) Cloning and/or expression vector containing a nucleic acid sequence according to claim 1.

20. (Original) Vector according to claim 19, characterized in that it includes the elements required for its expression in a host cell.

21. (Previously Presented) Host cell transformed with a vector according to claim 19.

22. (Original) Mammal, except a human, characterized in that it comprises a cell according to claim 21.

23. (Previously Presented) Mammal, except a human, according to claim 22, comprising a transformed cell, characterized in that the sequence of at least one of the two alleles of the SPG4 gene contains at least one of the mutations corresponding to a natural polymorphism in humans.

24. (Currently Amended) ~~Use~~ The use of a nucleic acid sequence according to claim 5, as a probe or primer, for detecting and/or amplifying nucleic acid sequences.

25. (Currently Amended) ~~Use~~ The use of a nucleic acid sequence according to claim 1, for screening a genomic or cDNA library.

26. (Previously Presented) Use of a nucleic acid sequence according to claim 1, for producing a recombinant or synthetic polypeptide.

27. (Original) Method for producing a recombinant polypeptide, characterized in that a transformed cell according to claim 21 is cultured under conditions which allow the expression of said recombinant polypeptide, and in that said recombinant polypeptide is recovered.

28. (Original) Polypeptide, characterized in that it is obtained using a method according to claim 27.

29. (Previously Presented) Monoclonal or polyclonal antibodies or their fragments, chimeric antibodies or immunoconjugates, characterized in that they are capable of specifically recognizing a polypeptide according to claim 14.

30. (Previously Presented) Method for detecting and/or purifying a polypeptide, characterized in that it uses an antibody according to claim 29.

31. (Currently Amended) ~~Method~~ A method for genotypic diagnosis of AD-HSP associated with the SPG4 gene, characterized in that a nucleic acid sequence according to claim 1 is used.

32. (Currently Amended) ~~Method~~ A method for genotypic diagnosis of AD-HSP associated with the presence of at least one mutation on a sequence of the SPG4 gene, using a biological sample from a patient, characterized in that it includes the following steps:

a) where appropriate, isolation of the genomic DNA from the biological sample to be analyzed, or production of cDNA from the RNA of the biological sample;

b) specific amplification of said DNA sequence of the SPG4 gene likely to contain a mutation, using primers according to claim 5;

c) analysis of the amplification products obtained and comparison of their sequence with the corresponding normal sequence of the SPG4 gene.

33. (Previously Presented) Method for diagnosing AD-HSP associated with abnormal expression of a polypeptide encoded by the SPG4 gene, characterized in that one or more antibodies according to claim 29 is brought into contact with the biological material to be tested, under conditions which allow the possible formation of specific immunological complexes between said polypeptide and said antibody, and in that the immunological complexes possibly formed are detected and/or quantified.

34. (Previously Presented) Method for selecting a chemical or biochemical compound which is capable of modulating the expression or the activity of a polypeptide encoded by the 5PG4 gene, characterized in that it comprises bringing a nucleic acid sequence according to claim 1 into contact with a candidate compound, and detecting a modification of the activity of said polypeptide.

35. (Previously Presented) Use of a nucleic acid sequence according to claim 1, for studying the expression or the activity of the SPG4 gene.

36. (Previously Presented) Kit for diagnosis, characterized in that it comprises at least a nucleic acid according to claim 5.

37. (Previously Presented) Method for selecting a chemical or biochemical compound which is capable of modulating the expression or the activity of a polypeptide encoded by the SPG4 gene, characterized in that it comprises bringing a nucleic acid sequence according to claim 14 into contact with a candidate compound, and detecting a modification of the activity of said polypeptide.

38. (Previously Presented) Use of a polypeptide according to claim 14 for studying the expression or the activity of the SPG4 gene.

39. (Previously Presented) Kit for diagnosis, characterized in that it comprises at least an antibody according to claim 29.

40. (Previously Presented) Use of an antibody according to claim 29 for studying the expression or the activity of the SPG4 gene.

41. (New) A method for detecting one or more polymorphisms in the SPG4 gene of a human biological sample, said method comprising:

a) amplifying DNA of the sample using one or more primers to obtain an amplification product,

b) sequencing the amplification product, and

c) comparing the DNA sequence of the amplification product with the DNA sequence of a wild-type SPG4 gene to identify one or more polymorphisms in the SPG4 gene of the sample.

42. (New) The method of claim 41, wherein the DNA is genomic DNA.

43. (New) The method of claim 41, wherein the DNA is cDNA.

44. (New) The method of claim 41, wherein the human biological sample is an antenatal human biological sample.

45. (New) The method of claim 41, wherein the human biological sample comprises lymphoblasts.

46. (New) The method of claim 41, wherein amplifying the DNA is performed by a method selected from the group consisting of polymerase chain reaction, strand

displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

47. (New) The method of claim 41, which uses at least one primer comprising any of SEQ ID Nos. 4-71.

48. (New) A method for detecting one or more polymorphisms in the SPG4 gene of a human biological sample, said method comprising:

a) amplifying DNA of the sample with one or more primers to obtain an amplification product;

b) hybridizing the amplification product with a probe that hybridizes specifically with the DNA of a wild-type SPG4 gene, to produce a hybridized DNA; and

c) applying a method to detect one or more mismatches in the hybridized DNA to identify one or more polymorphisms in the SPG4 gene of the sample.

49. (New) The method of claim 48, wherein the DNA is genomic DNA.

50. (New) The method of claim 48, wherein the DNA is cDNA.

51. (New) The method of claim 48, wherein the human biological sample is an antenatal human biological sample.

52. (New) The method of claim 48, wherein the human biological sample comprises lymphoblasts.

53. (New) The method of claim 48, wherein amplifying the DNA is performed by a method selected from the group consisting of polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

54. (New) The method of claim 48, wherein the probe comprises any of SEQ ID Nos. 4-71.

55. (New) A method for diagnosing the presence or absence of an autosomal dominant hereditary spastic paraplegia in a human, wherein the autosomal dominant hereditary spastic paraplegia is associated with the presence of a mutation in the SPG4 gene, the method comprising detecting the presence or absence of one or more mutations in the SPG4 gene in a biological sample obtained from the human.

56. (New) The method of claim 55 wherein detecting the presence or absence of one or more mutations in the SPG4 gene comprises amplifying DNA of the biological sample obtained from the human using primers, determining the DNA sequence of the amplified product, and comparing the DNA sequence of the amplified product with the DNA sequence of a wild-type SPG4 gene to detect one or more mutations in the SPG4 gene in the biological sample.

57. (New) The method of claim 56, wherein the DNA is genomic DNA.

58. (New) The method of claim 56, wherein the DNA is cDNA.

59. (New) The method of claim 56, wherein the biological sample is an antenatal human biological sample.

60. (New) The method of claim 56, wherein the biological sample comprises lymphoblasts.

61. (New) The method of claim 56, wherein amplifying the DNA is performed by a method selected from the group consisting of polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

62. (New) The method of claim 56, which uses at least one primer comprising any of SEQ ID Nos. 4-71.

63. (New) The method of claim 55, wherein detecting the presence or absence of a mutation in the SPG4 gene comprises amplifying DNA of the biological sample obtained from the human, hybridizing the amplified product with a probe that hybridizes specifically with the DNA of a wild-type SPG4 gene, applying a method to detect the presence of mismatches in the hybridized DNA, wherein the detection of one or more mismatches indicates one or more mutations in the SPG4 gene in the biological sample.

64. (New) The method of claim 63, wherein the DNA is genomic DNA.

65. (New) The method of claim 63, wherein the DNA is cDNA.

66. (New) The method of claim 63, wherein the biological sample is an antenatal human biological sample.

67. (New) The method of claim 63, wherein the biological sample comprises lymphoblasts.

68. (New) The method of claim 63, wherein amplifying the DNA is performed by a method selected from the group consisting of polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

69. (New) The method of claim 63, which uses at least one probe comprising any of SEQ ID Nos. 4-71.

70. (New) A method of determining the presence or absence of autosomal dominant hereditary spastic paraplegia in a human, wherein the autosomal dominant hereditary spastic paraplegia is associated with the presence of a mutation in the SPG4 gene in a human, said method comprising determining the presence or absence of one or more mutations in the SPG4 gene in a biological sample obtained from the human.

71. (New) The method of claim 70, wherein the mutation is identified using at least one nucleic acid comprising any of SEQ ID Nos. 4-71.